SYNOPSIS OF RESEARCH PROJECT

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9. Introduction

Oilseed crops play a crucial role in India's agricultural economy, ranking just after cereals in overall production. The main oilseeds grown in the country include seven edible types namely groundnut, rapeseed-mustard, soybean, sunflower, safflower, sesame and niger and two non-edible ones, castor and linseed. Among these, castor (*Ricinus communis* L.) is a significant non-edible oilseed crop cultivated in arid and semi-arid regions of tropical and subtropical areas worldwide. It belongs to the genus *Ricinus* in the Euphorbiaceae family. Castor is a cross-pollinated crop with a chromosome number of 2n=20. Under natural conditions, cross-pollination can exceed 80%, although the actual rate depends on the genotype and environmental factors (Setayeshnasab *et al*., 2025).

The plant is monoecious, with its inflorescence forming a raceme or spike. Female flowers occupy 50-70 per cent of the upper portion of the raceme, while male flowers make up 30-50 per cent of the lower portion. *Ricinus communis* is reported to be a secondary balanced polyploid with a basic chromosome number of x=5. Haploid studies indicate that the species originated as a tetraploid derived from diploid

progenitors (2n=10). Wild species of castor include *Ricinus perciens*, *Ricinus chinesis* and *Ricinus maxicanus* (Kulkarni, 1959).

Castor is thought to have originated primarily in the Ethiopian-East African region. There are four recognized centres of diversity for castor, namely: Ethiopia-Eastern Africa, North-West and South-West Africa with the Arabian Peninsula, the Indian subcontinent and the Chinese subcontinent.

Castor is a sexually polymorphic plant and naturally occurring castor is predominantly monoecious. The main sex forms include monoecious, pistillate, pistillate with interspersed staminate flowers (IFS) and sex revertants (Shifriss, 1960). The expression of sex in castor is strongly affected by environmental factors. Lower temperatures (below 30°C) and higher nutrient availability encourage the development of female flowers, increasing femaleness on a spike. In contrast, higher temperatures (above 32°C), later-order spikes and low nutrition favor the production of male flowers on a spike (Lavanya, 2002).

Castor seeds contain about 47-55 per cent oil and 18 per cent protein. The oil is a colorless to pale yellow liquid with little to no odor or taste. What makes castor oil distinctive is that nearly 90 per cent of its composition consists of a single fatty acid, ricinoleic acid. The presence of this 12-hydroxy fatty acid with 18-carbon chain gives castor oil its unique physical and chemical properties. Unlike most other oils, castor oil is soluble in alcohol, has high viscosity, and requires less heating during biodiesel production (Yadava *et al*., 2011).

Castor oil has significant industrial importance and is extensively used in the manufacture of lubricants, greases, wax blends, plastics, nylon, hydraulic fluids, artificial leather, rubber, printing inks, soaps, fast-drying oils, paints, varnishes, ricinoleic acid and candles. Refined castor oil also has strong demand in domestic markets, particularly for medicinal purposes and as a preservative for stored grains. Unlike most vegetable oils, castor oil does not solidify even at very low temperatures of -12°C to -18°C, which makes it an excellent lubricating agent, especially for high-speed engines and aircraft.

Castor cake is a valuable by-product obtained after the extraction of oil. It is rich in essential plant nutrients, particularly nitrogen, along with phosphorus and potassium, making it an effective organic fertilizer for a wide range of crops. Castor cake improves soil fertility, enhances microbial activity, and supports healthy plant

growth. Although it has high nutritional value, its use as animal feed is restricted because it contains toxic compounds such as ricin.

India remains the top global producer of castor, ranking first in both cultivation area and production. In 2024-25, castor was grown over 9.65 lakh hectares in India, producing 17.86 lakh tons with a productivity of 1851 kg/ha (Anonymous, 2025a). Indian castor productivity exceeds the world average and is the highest among major producing countries including China, Brazil and Thailand.

The primary castor-growing states in India include Gujarat, Rajasthan, Telangana, Andhra Pradesh, Karnataka, Tamil Nadu and Odisha. In Gujarat, during 2024-25, castor was cultivated on 6.46 lakh hectares, producing 14.03 lakh tons with an average productivity of 2171 kg/ha (Anonymous, 2025b). Productivity of Gujarat state surpasses that of other states, largely because most of its cultivation area is planted with hybrid varieties. The major castor-producing districts in Gujarat are Banaskantha, Mehsana and Sabarkantha.

Several factors contribute to the low yields under rainfed conditions, including monocropping on marginal and sub-marginal lands, unpredictable and uneven rainfall, delayed sowing and poor crop management with minimal or no inputs. In addition, castor production is severely affected by various diseases, with Botrytis grey rot and Fusarium wilt being the most destructive. Wilt is a soil and seed born disease caused by *Fusarium oxysporum* f. sp. *ricini*. It is a one of the most destructive disease of castor in India, causes severe yield losses and widespread crop damage (Nanda and Prasad (1974; Dange *et al*., 1997). In wilt-endemic regions, disease incidence can reach as high as 85-90 per cent and even the widely grown wilt-resistant hybrids have shown breakdown of resistance. Therefore, release of any hybrid or variety at state or national level in India, it should be wilt resistant, in addition to having high seed yield and desirable yield-attributing characteristics.

The phenomenon of heterosis has been found to be the most important genetic tool for improvement of seed yield in cross-pollinated species in general and particularly in castor. Exploitation of hybrid vigor in castor has been possible only due to availability of pistillate lines in castor (Gopani *et al.*, 1968). In Gujarat, breakthrough in castor production has been achieved through the development and release of hybrids for commercial cultivation. Gujarat was first in the creation and introduction of commercial hybrids. Series of hybrids *viz*., GCH-3, GAUCH-1, GCH-2, GCH-4, GCH-

5, GCH-6, GCH-7, GNCH-1, GCH-8, GCH-9 and GCH-10 have been released for commercial cultivation in Gujarat.

Selection of plants according to phenotypic traits of quantitative characters is not much effective because of presence of genotypic-environment interaction. Hence knowledge regarding heterosis (hybrid vigor) and inbreeding depression become important for a successful breeding programme. The knowledge regarding heterosis (hybrid vigor) for yield and its components gave an idea about the possibility for the enhancing seed yield either by developing hybrids or to isolate genotypes from segregating population of high heterotic hybrids.

10. Practical utility

Line × tester mating design is well suited for crops like castor, as it allows partitioning of genetic variance into additive and non-additive components, making it useful for studying polygenic inheritance (Kempthorne, 1957). This method is effective for evaluating vast number of parents and crosses based on their combining ability.

Exploitation of hybrid vigor is a major achievement in this crop. In heterosis breeding, it is important to evaluate diverse and promising parental genotypes and their hybrids for seed yield performance and associated traits. Identifying superior hybrids based on the extent and direction of heterosis is crucial. Knowledge of the magnitude and nature of prevalent genetic variation is helps to assess the genetic potential of a population.

Combining ability studies help in identifying good parental lines that can produce superior hybrids or segregants. They also offer insights into the nature and magnitude of gene action governing seed yield and its contributing traits, which is useful for planning future breeding programmes.

Information on the degree of heterosis, combining ability and the nature of gene action governing seed yield and its component traits is helpful in selecting suitable parents for the development of superior cross combinations. Such knowledge also aids in commercially utilizing hybrid vigor and designing effective breeding programmes for castor improvement.

Phenotypic expression can be described as a linear function of genotype (G), environment (E) and their interaction (G × E). The relative contribution of these main and interaction effects differs among genotypes (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Perkins and Jinks, 1968). Analysis of G × E interaction provides

valuable guidance in identifying suitable genotypes for specific environmental niches. Assessment of stability parameters across environments facilitates the identification of genotypes with stable, high yield and consistent performance of yield-related traits, which is particularly important for rainfed castor cultivation under variable environmental conditions.

Studying the inheritance pattern of Fusarium wilt resistance in the F_2 generation helps in understanding the inheritance pattern of resistance, including whether it is influenced by additive or non-additive gene action (dominant, recessive or epistasis). This information is useful for identifying resistant segregants in early generations and for choosing suitable breeding strategies. It also assists breeders in developing wilt-resistant varieties by selecting appropriate parents and efficiently advancing promising lines, thereby reducing yield losses and improving crop stability.

11. Objectives

Considering the various aspects discussed above and recognizing the need for a comprehensive study in castor, the present investigation on "Genetic architecture of seed yield, its components and Fusarium wilt resistnce in castor (*Ricinus communis* L.)" will be undertaken with the following major objectives:

1. To assess the extent of heterobeltiosis and standard heterosis for seed yield and its contributing traits
2. To estimate the general combining ability of parents and specific combining ability of crosses for seed yield and its contributing traits
3. To study the nature of gene action associated with the inheritance of seed yield and its contributing traits
4. To estimate genotype × environment interaction and stability parameters of parents and its crosses for seed yield and its contributing traits
5. To study the inheritance pattern of Fusarium wilt resistance in F_2 generation along with F_1 and its parents of selected crosses

12. Review of literature

The literature relevant to the present investigation has been reviewed under the following sub-headings:

12.1 Heterosis

12.2 Combining ability and gene action

12.3 Genotype × environment interaction and stability analysis

12.4 Inheritance pattern of Fusarium wilt resistance

12.1. Heterosis

Heterosis is the phenomenon where an F_1 hybrid shows increased or decreased performance compared to the average of its parents (mid-parent heterosis or relative heterosis). First observed by Koelreuter (1766), its practical use began in maize and later extended to crops like bajra, cotton, castor and sorghum. Shull (1908) coined the term heterosis, attributing it to heterozygosity. Fonseca and Patterson (1968) introduced heterobeltiosis, referring to superiority over the better parent, while Meredith and Bridge (1972) defined standard heterosis as superiority over a standard variety or hybrid.

Joshi *et al*. (2002a) evaluated heterobeltiosis and standard heterosis for seed yield and associated traits across four environments using 112 castor hybrids generated through a line × tester mating design (4 × 28). The crosses SKP-93 × J-1 (87.89 and 107.04 %, respectively), SKP-93 × 6-219-22 (84.82 and 88.35 %, respectively) and VP-1 × HO (80.48 and 94.80 %, respectively) showed positive and significant heterosis over both BP and SH for seed yield per plant. These hybrids also expressed positive and significant heterosis for yield-related attributes, including number of capsules per plant, number of capsules on the main spike and seed yield per main spike. Significant and positive heterosis over BP and SH was observed for days to flowering, days to maturity of the primary spike, plant height up to the primary spike, number of nodes up to the primary spike, length of the primary spike, number of effective branches per plant and 100-seed weight (g). In contrast, heterosis observed for oil content (%) was comparatively low.

Thakkar *et al.* (2005) evaluated 75 castor hybrids developed through a line × tester mating design involving five female and fifteen male parents across four environments. Positive and significant heterobeltiosis (HB) and standard heterosis (SH) in terms of seed yield per plant were recorded from 5.57 to 128.46 per cent 3.58 to 28.98 per cent, respectively. Top five best-performing crosses for seed yield per plant based on per se, heterobeltiosis and standard heterosis included SKP-49 × SPS-43-3, Geeta × SKI-147, SKP-49 × SH-72, SKP 49 × SKI 180 and GEETA × HC 8. Moreover, these hybrids exhibited positive heterosis for number of capsules per plant, capsules on primary raceme, effective length of primary raceme, earliness and oil content (%).

Golakia *et al.* (2008) evaluated forty-four castor hybrids developed by line × tester mating design (four pistillate lines × 11 male parents) along with parental lines and a standard check for heterosis of yield determinant characters. Heterosis over better parent ranged from 18.74 to 39.57 per cent and standard heterosis ranged from 16.98 to 32.83 per cent for seed yield per plant. The highest heterosis over better parent (BP) was recorded for number of capsules per plant (54.9%) followed by seed yield per plant (39.6%) and effective branches per plant (18.7%). However, the maximum standard heterosis (SH) was expressed by number of effective branches per plant (44.88%) followed by effective length of main raceme (34.76%), 100-seed weight (33.21%) and seed yield per plant (32.83%). Cross JP 65 × JI 309 was best in terms of heterobeltiosis (39.57%) and JP 88 × DCS 89 was superior according to standard heterosis (32.83%) for seed yield per plant.

Chaudhari *et al.* (2011) evaluated 10 diverse inbred lines and their 45 crosses generated by half-diallel mating design along with two standard checks *viz.,* GCH-4 and GCH-5 across four environments to assess the magnitude of heterosis for seed yield and its related component traits. Heterobeltiosis (HB) and standard heterosis (SH) over GCH-4 and GCH-5 for seed yield per plant over different environments varied between -13.71 to 47.89 per cent, -25.08 to 22.77 per cent and -31.62 to 12.04 per cent, respectively. Cross SKI-232 × DCS-9 (22.77%) produced a significantly higher yield than GCH-4 while, none of the crosses showed significantly superior over best check hybrid GCH-5 across all the environments. Across the environments, heterobeltiosis for days to 50 per cent flowering varied between -15.60 to 46.58 per cent, while it was -15.00 to 23.23 per cent for days to maturity, -8.18 to 28.14 per cent for number of nodes per plant -16.16 to 61.65 per cent for plant height.

Chaudhari and Patel (2014) evaluated 32 castor hybrids developed using line × tester mating design. Hybrids VP 1 × ANDCM 2 (14.03%), SKP 84 × ANDCM 2 (13.30%) and VP 1 × ANDCI 2 (12.16%) were recognized as promising crosses demonstrating high heterosis and superior mean performance for seed yield and related yield traits. Desirable negative standard heterosis (SH) for days to 50 per cent flowering and days to maturity was recorded in the cross VP 1 × ANDCI 9 (-19.71% and -10.04%, respectively). Additionally, crosses JP 65 × ANDCM 2 (7.95%), VP 1 × SKI 215 (7.21%) and Geeta × ANDCI 8 (6.83%) showed high positive standard heterosis (SH) for oil content.

The diallel analysis was conducted by Makani *et al*. (2015) using 10 genetically diverse parental lines and their 45 F_1 hybrids in four different environments to study heterosis in castor. The heterobeltiosis (HB) for seed yield per plant varied from -44.48 per cent (MCI 108 × SKI 337) to 30.61 per cent (SKI 341 × GC 3) in E_1, -58.72 per cent (MCI 108 × SPS 35-50) to 39.98 per cent (SH 41 × SKI 337) in E_2, -33.37 per cent (1379 × SKI 307) to 25.10 per cent (SKI 341 × GC 3) in E_3 and -48.64 per cent (MCI 108 × 1379) to 45.14 per cent (MCI 108 × GC 3) in E_4. For seed yield per plant, hybrids MCI 108 × SKI 341 and SKI 341 × SPS 43-3 showed significant positive standard heterosis over the check hybrid GCH 7 in all environments, while SKI 341 × GC 3 and MCI 108 × GC 3 showed positive and significant standard heterosis (SH) in a minimum of two environments only. The standard heterosis (SH) for days to 50 per cent flowering varied across environments, ranging from -23.16 to 16.38 per cent in E_1, -14.62 to 18.13 per cent in E_2, 19.53 to 10.06 per cent in E_3 and -15.48 to 13.69 per cent in E_4.

Sapovadiya *et al.* (2015a) a investigated the magnitude of heterosis across environments for twelve quantitative traits including seed yield per plant, in castor. A total of 52 crosses were produced by crossing four pistillate lines with 13 monoecious lines using a line × tester crossing design. For seed yield per plant, significant desirable heterobeltiosis (HB) varied from -37.14 to 75.95 per cent, while standard heterosis (SH) ranged from -61.77 to 18.64 per cent. However, the extent of heterosis varied considerably among different crosses and traits. In the pooled analysis, the crosses JP-89 × PCS-124, JP-89 × RG-2826, SKP-84 × 48-1, SKP-106 × 48-1, and SKP-106 × PCS-124 showed the highest heterosis for seed yield per plant with heterobeltiosis of 75.95%, 70.45%, 61.11%, 60.45% and 58.57%, respectively. The heterosis observed in seed yield per plant corresponded to the heterosis shown by its individual component traits.The magnitude of heterosis were high for seed yield per plant, plant height up to primary raceme, number of effective branches per plant and number of capsules on primary raceme; moderate for days to 50 per cent flowering of primary raceme, days to maturity of primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme and 100-seed weight (g) and low for shelling out-turn (%) and oil content (%).

Patted *et al*. (2016) studied heterobeltiosis (HB) and standard heterosis (SH) for seed yield and component traits in 80 castor hybrids developed through a line ×

tester experimental design involving 10 lines and 8 testers. Positive and significant heterosis for seed yield over the better parent ranged from -35.15 to 111.34 per cent, while standard heterosis over the checks DCH 177 and DCH 519 ranged from -46.89 to 48.14 per cent and -27.72 to 101.63 per cent, respectively. The hybrid DCS 94 × K 11-1166-11 recorded the highest positive and significant heterosis over the better parent (111.34%) and also exhibited significant positive standard heterosis (SH) over both checks DCH 177 (48.14%) and DCH 519 (101.63%) for seed yield per plant.

Delvadiya *et al*. (2018) evaluated 72 castor hybrids developed through a line × tester mating design involving 4 lines and 18 testers for twelve quantitative traits. The measured heterobeltiosis (HB) and standard heterosis (SH) over standard check (SC) hybrid GCH-9 were ranged from -33.80 to 8.60 per cent and -31.86 to 0.98 per cent for days to flowering of primary raceme, -24.39 to 6.34 per cent and -24.57 to 9.25 per cent for days to maturity of primary raceme, -52.45 to 45.19 per cent and -59.44 to 80.77 per cent for plant height up to primary raceme, -32.97 to 27.15 per cent and -30.71 to 27.42 per cent for number of nodes up to primary raceme, -47.60 to 32.15 per cent and -23.46 to 55.04 per cent for length of primary raceme, -47.14 to 31.16 per cent and -23.80 to 56.58 per cent for effective length of primary raceme, -57.52 to 44.53 per cent and -38.25 to 57.77 per cent for number of effective braches per plant, -53.64 to 73.48 per cent and -45.74 to 79.65 per cent for number of capsules on primary raceme, -24.76 to 22.88% and -21.54 to 22.56 per cent for shelling out turn, -39.55 to 24.76 per cent and -19.23 to 67.95 per cent for 100-seed weight (g), -44.56 to 115.85 per cent and -61.90 to 52.45 per cent for seed yield per plant and -2.94 to 1.30 per cent and -2.45 to 1.76 per cent for oil content, respectively.

Barad *et al*. (2019) evaluated 101 entries, comprising 10 parents, 45 hybrids (F_1) developed using a half-diallel mating design, their 45 F_2 progenies and a standard check (GCH 7). They found that the extent of standard heterosis (SH) in positive direction was high in number of effective branches per plant and seed yield per plant, medium for 100-seed weight (g), effective length of the primary raceme and length of the primary raceme and low for oil content (%). Conversely, the magnitude of negative standard heterosis was high for the number of nodes up to the primary raceme and plant height while, medium for days to maturity of the primary raceme and days to 50 per cent flowering of the primary raceme. The cross JI 368 × RG 2787 exhibited the highest

significant positive heterobeltiosis (51.08%), standard heterosis (40.15%) and also recorded the highest seed yield per plant (486.80 g).

An experiment was conducted by Yamanura *et al*. (2020) to assess the nature and magnitude of heterosis with respect to seed yield and the associated component traits in castor. They produced 40 hybrids by crossing five lines with eight testers using a line × tester mating design. The highest level of standard heterosis (SH) for seed yield per plant occurred in the hybrid VP 1 × RG 109 (260.05%). For the yield components, the highest value of standard heterosis (SH) recorded was 178.45 per cent (VP 1 × RG 3160) for effective length of the primary raceme, 230.23 per cent (DPC 9 × RG 3160) for the number of capsules on the primary raceme, 308.08 per cent (DPC 9 × RG 2661-1) for the number of effective spikes per plant, 35.35 per cent (DPC 9 × RG 109) for 100-seed weight (g), 24.04 per cent (VP 1 × RG 3160) for volume weight and 4.32 per cent (DPC 18 × RG 72) for oil content. Top three hybrids showing the highest standard heterosis for seed yield per plant were VP 1 × RG 109 (260.05%), DPC 18 × RG 1771 (236.80%) and DPC 18 × RG 2661-1 (235.80%).

A study was carried out by Delvadiya *et al*. (2021) to investigate heterosis in seed yield and its related component traits in castor. The heterobeltiosis was found in a favorable direction for total length of primary raceme (4.73%), effective length of primary raceme (4.73%), shelling out turn (1.25%), 100-seed weight (0.94%) and seed yield per plant (23.01%) in JM 6 × 48-1and for days to maturity of primary raceme (-7.07%), plant height up to primary raceme (-7.13%), number of nodes up to primary raceme (-0.87%), number of capsules on primary raceme (2.87%), shelling out turn (1.70%) and oil content (0.68%) in JI 436 × PCS 124.

Nivedha *et al*. (2023) estimated magnitude of heterosis in 30 castor crosses developed through line × tester mating design. The estimation of standard heterosis ranged from -17.28 to 60.49 per cent for days to 50 per cent flowering, -8.19 to 28.65 per cent for days to maturity, -38.74 to 38.11 per cent for plant height, -13.60 to 87.20 per cent for number of nodes up to the primary raceme, -64.52 to 106.99 per cent for number of effective spikes per plant, -27.84 to 49.19 per cent for effective length of the primary spike, -23.77 to 30.66 per cent for 100-seed weight, -5.00 to 5.58 per cent for oil content and -56.86 to 130.57 per cent for seed yield per plant.

Chaudhary *et al*. (2024) determined heterosis among 20 crosses of castor. The highest value of heterobeltiosis was 67.12% and standard heterosis (SH) were 38.98,

32.37 and 33.66% compared to GNCH 1, GCH 8 and GCH 9, respectively for seed yield per plant in cross NAUCI 8 × NAUCI 7. Three cross combinations *viz*., NAUCI 8 × NAUCI 7, NAUCI 6 × NAUCI 8 and NAUCI 9 × NAUCI 3 exhibited positive and significant standard heterosis (SH) compared to the checks GNCH 1, GCH 8 and GCH 9. The highest heterotic cross NAUCI 8 × NAUCI 7 also exhibited highest percentage of standard heterosis (SH) in favorable direction for yield attributing characters like number of secondary branches per plant, number of nodes up to primary spike, days to maturity and oil content (%).

Pandor *et al*. (2025a) evaluated 61 castor genotypes comprising three diverse pistillate lines, fourteen testers, forty-two crosses developed using a line × tester mating design and two standard check (SC) hybrids GCH 7 and GNCH 1. Heterosis over better parent (Heterobeltiosis) ranged from -52.95 (VP 1 × ANDCI 10-3) to 78.91 (Geeta × SKI 343) per cent; while, standard heterosis over better check GCH 7 varied from -55.58 (VP 1 × ANDCI 10-5) to 70.89 (Geeta × SKI 315) per cent. Total 13 and 9 hybrids exhibited positive and significant heterobeltiosis and standard heterosis over best check for seed yield per plant, respectively. Top five cross combinations exhibited higher estimate of heterobeltiosis (HB) and standard heterosis (SH) for seed yield per plant were Geeta × SKI 343, Geeta × SKI 315, Geeta × ANDCI 12-2, SKP 84 × ANDCI 14 and Geeta × SKI 215.

12.2. Combining ability and gene action

In castor breeding, high-yielding parents do not always produce superior hybrids, so selecting parents based only on their own performance is often unreliable. Instead, choosing lines based on their ability to transmit desirable traits to their progeny is more effective. Combining ability analysis helps to identify such parents. Davis (1927) introduced top-crossing to evaluate inbred lines and Sprague and Tatum (1942) later defined general combining ability (GCA) as average hybrid performance and specific combining ability (SCA) as the outcome of specific crosses due to non-additive gene effects.

Joshi *et al*. (2002b) examined the combining ability of 32 castor parental lines (4 pistillate lines and 28 male lines) and their 112 F_1 hybrids, which were produced using a line × tester mating design across four different environments. The parent SKP was identified as a good general combiner for seed yield per plant, seed yield per main spike, number of capsules per main spike, 100-seed weight (g) and oil content (%).

Some other lines *viz*., SH 41, HO, T4, SH 21 and 2-73-11 were also found good general combiners for seed yield per plant. A significant positive association was observed between parental trait performance and their general combining ability for several traits. The crosses SKP 93 × J1, SKP 93 × 6-219-22 and VP 1 × HO showed high specific combining ability for seed yield per plant.

Tank *et al*. (2003) evaluated ten inbred lines *viz*., JI-122, SKI-131, JI-106, JI-226, JI-265, SKI-121, DCS-9, 48-1, GC-2 and SKI-80 and their 45 F_1 hybrids in four artificially created environments. The environments were created using two sowing dates (30 July and 30 August). Analysis of combining ability across different environments revealed significant variances in both general and specific combining abilities for all the traits examined. Most traits were mainly governed by non-additive gene effects, except for effective length of the main raceme and number of capsules on the main raceme. The parents 48-1, DCS-9 and JI-106 were recognized as good general combiners for seed yield, while the cross SKI-80 × JI-226 showed high *per se* performance and sca effect.

Madariya *et al*. (2008) conducted a combining ability study using a line (10) × tester (4) mating design across four different environments. The pooled analysis showed that GCA and SCA variances were strongly affected by environments suggested that the parent genotypes and crosses must be evaluated in wide range of environments for unbiased estimates. The results of the analysis of variance suggested that non-additive gene action mainly controlled seed yield per plant, in contrast to other studied traits, which were more affected by additive gene action. The parents JP 84 (11.81), JP 88 (5.56), JI 285 (27.19), SKI 226 (24.21) and JI 306 (20.19) were good general combiners for seed yield per plant and some yield contributing traits. Parent SKP 106 was good general combiners for number of capsules per plant (1.70) and oil content (0.14), while JP 65 was good general combiner for 100-seed weight (0.65). Three crosses *viz.*, JP 84 × JI 285, JP 88 × JI 285, JP 84 × JI 306 and SKP 106 × JI 257 were good specifics combiners for seed yield per plant which involved either average or good general combiner parents.

Sridhar *et al*. (2010) investigated the combining ability of lines and testers for earliness and related traits across different environments using a line × tester design with five lines and fifteen testers. Analysis of GCA and SCA indicated that additive gene action predominated for the number of nodes up to the primary spike, while non-

additive gene action governed plant height. Whereas, days to 50 per cent flowering and days to maturity were governed by both additive and non-additive gene actions, as indicated by comparable GCA and SCA variances. Kranthi, RG-1471, RG-178, DCS-9 and RG-2724 were recognized as good general combiners for all four traits. The crosses Kranthi × RG-1471, LRES-17 × RG-2724 and VP-1 × RG-1471 were most specific combiners for the majority of earliness-related traits.

Patel *et al*. (2012) studied combining ability in castor using 48 hybrids derived from 16 parents (four females and twelve males) through a line × tester mating design across environments. The potence ratio (σ^2GCA/σ^2SCA) estimates revealed that additive genetic variance was predominant for traits such as days to 50 per cent flowering, number of nodes up to the primary spike, effective length of the primary spike, total number of capsules per plant, seed yield per plant and 100-seed weight (g). Non-additive genetic variance played the major role in determining the number of days to 50% maturity of the primary spike and shelling out turn, while for number of capsules on the primary spikes, only additive genetic variance was significant. Additive genetic variance was more stable across environments for all traits, whereas non-additive variance showed environmental variation for all characters except shelling out turn and oil content (%). The pistillate parents SKP 84 (21.18) and GEETA (16.88), along with the male lines SKI-270 (68.14), DCS-47 (24.24), SPS-44-1 (15.76), EB-16 (12.09) and SKI-147 (8.21) were found to be good general combiners for seed yield and its major contributing traits. The crosses SKP-24 × SKI-270 (81.76), VP-1 × DCS-47 (57.25) and SKP-84 × SKI-202 (53.01) showed high specific combining ability for seed yield per plant.

Kasture *et al*. (2014) conducted a line × tester analysis in castor using 40 hybrids developed from 10 inbred lines and 4 diverse pistillate lines to evaluate seed yield and related traits. The analysis of GCA and SCA variances revealed that additive gene action played a major role in controlling traits like plant height, number of nodes up to the primary spike, days to 50 percent flowering, days to maturity and oil content (%). Within the parental lines, Geeta (14.83), SKP 84 (5.33), DCS 84 (11.92), DCS 85 (9.44) and JI 381 (23.01) were found to be good general combiners for seed yield per plant and several other yield-related traits. Considering the SCA effects of hybrids, JP 65 × JI 381 (55.90), VP 1 × DCS 97 (34.05) and Geeta × DCS 85 (33.22) were recognized as the most promising cross combinations for seed yield per plant.

Sapovadiya *et al*. (2015b) studied combining ability for seed yield and associated traits in castor across three environments using four pistillate lines, thirteen monoecious testers, their resultant 52 F_1 hybrids and check hybrid GCH-7. Analysis of variance indicated that 100-seed weight (g) was largely governed by additive gene action, whereas non-additive gene action was predominated for traits such as days to 50 per cent flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, shelling out-turn, seed yield per plant and oil content (%). One line, *viz*., JP-89 and five testers, viz., PCS-124, DCS-85, SKI-215, JI-353 and JI-357 were identified as good general combiners for seed yield per plant, owing to the significant positive GCA effects reflecting a high number of favorable genes. Twelve crosses were identified as good specific combiners for seed yield per plant, with the cross JP-96 × PCS-124 showing the highest SCA effect.

Patel *et al*. (2016) evaluated a total of 56 genotypes, comprising 6 pistillate lines, 7 inbred lines, and 42 hybrids produced using a line × tester mating design, along with the standard check GCH-7. Analysis of general combining ability (GCA) and specific combining ability (SCA) variances variance indicated that non-additive gene action predominated for most traits, including days to flowering, days to maturity, plant height up to the primary spike, length of primary spike, seed yield per plant, effective spikes per plant, oil content (%) and number of nodes up to the primary spike while, Additive gene action was found to be predominant for 100-seed weight (g) and number of capsules on the primary spike. Parents SKP 106 (0.20) and SKI 350 (0.43) were found to be as good general combiners for seed yield per plant, while SKP 121, SKP 122 and JP 96 were found to be good general combiners for days to flowering, days to maturity and effective branches per plant. Several hybrids showed significant and desirable SCA effects for traits such as days to flowering (31), days to maturity (35), plant height up to primary spike (2), 100-seed weight (g) (1), seed yield (6), length of primary spike (1), number of nodes up to the primary spike (1), number of capsules on primary spike (2), oil content (%) (19) and effective branches per plant (6). Hybrids JI 96 × SKI 350 (1.09) and SKP 121 × SH 41 (0.86) were found to be good specific combiners for seed yield per plant.

Patel *et al*. (2017) examined combining ability in castor and found that the inheritance of the traits studied is influenced by both additive and non-additive gene effects. Among the parental lines, ANDCI 10-12, ANDCI 8, ANDCI 10-4 and ANDCI 10-3 were found to be as good general combiners for seed yield per plant, length of the primary raceme, effective length of the primary raceme, total number of capsules on the primary raceme and total number of capsules per plant. The crosses ANDCI 10-1 × ANDCI 9, ANDCI 10-12 × ANDCI 10-11, ANDCI 8 × ANDCI 10-3 and ANDCI 8 × ANDCI 10-11 showed positive and significant SCA effects for seed yield and its associated component traits.

Panera *et al*. (2018) investigated combining ability of castor using ten diverse parents along with their 45 F_1 hybrids developed through a half-diallel mating design for twelve quantitative and quality traits. Analysis of variance revealed that mean squares for both GCA and SCA were significant for all traits except SCA for oil content (%), indicating that both additive and non-additive gene effects played a significant role in the inheritance of the studied characters. The estimates of σ^2GCA were higher than σ^2SCA for effective length of the primary raceme and oil content (%), suggesting the predominance of additive genetic variance for these traits. In contrast, non-additive genetic variance played a predominant role in number of capsules on the primary raceme, number of effective branches per plant, shelling outturn, 100-seed weight (g) and seed yield per plant. Among the parents, PCS 124, SKI 215 and JI 35 were recognized as good general combiners for seed yield per plant and other yield-contributing traits. Out of ten top high-yielding hybrids, four crosses *viz*., SKP 84 × PCS 124 (207.46), VP 1 × SKI 346 (152.48), SKP 84 × JI 35 (136.72) and VP 1 × JI 368 (132.14) also exhibited significant and desirable SCA effects for seed yield per plant, which involved combinations of poor × good, average × average, poor × good and average × average general combiners, respectively.

Madariya *et al*. (2020) investigated combining ability in castor by crossing five pistillate lines with 13 monoecious lines to study seed yield and related component traits. The results indicated that variances for both GCA and SCA were significant for all traits, highlighting the role of both additive and non-additive gene actions. Non-additive gene action played a predominant role for seed yield and oil content (%), whereas additive gene action was predominant for traits like length of the main spike, number of capsules on the main spike, number of effective spikes per plant and 100-

seed weight (g). Three pistillate lines JP 96 (1.10), JP 106 (8.21) and SKP 84 (2.84) and five male lines JI 454 (3.04), JI 455 (4.56), JI 456 (3.01) and JI 457 (8.65) were found to be good general combiners for seed yield and its associated traits. Crosses JP 96 × JI 457, JP 96 × JI 462, SKP 84 × JI 455, DPC 15 × JI 454 and JP 96 × JI 455 showed high per se performance along with good or average specific combining ability (SCA) effects for seed yield.

An experiment was conducted by Mohanty *et al*. (2021) involving 40 entries which included 2 pistillate lines, 12 monoecious lines, their 24 hybrids produced using a line × tester design and two check hybrids. The study showed that σ^2GCA was higher than σ^2SCA for days to 50 per cent flowering of the primary raceme, days to maturity of the primary spike, plant height up to the primary spike, number of nodes up to the primary spike and 100-seed weight (g) which indicated additive gene action was the major contributor to the inheritance of these traits. In contrast, σ^2SCA exceeded σ^2GCA for total length of the primary spike, effective length of the primary spike, number of effective spikes per plant, number of capsules on the primary spike and seed yield per plant indicating that non-additive gene action predominates for these traits. On the basis of GCA effects, the parental lines DCS 102 (-5.23), DPC 23 (-3.09), DCS 64 and DCS 105 (-3.01) were found to be good general combiners for earliness, while DCS 110 (19.19), DCS 112 (14.13) and M 571 (2.88) were found to be good combiners for seed yield per plant and its associated traits like number of capsules on the primary spike and 100-seed weight (g). These parental lines can be effectively used in hybridization programs for enhancement of the respective traits. Within the hybrids, DPC 23 × DCS 123 (13.88) and M 571 × DCS 105 (12.28) exhibited high and desirable SCA effects for seed yield per plant and one or more component traits.

Nivedha *et al*. (2023) work out combining ability and gene action in castor using a line × tester analysis involving 6 lines and 5 testers. The analysis of genetic variances indicated that dominant gene action was predominant for most traits, except for oil content (%) and 100-seed weight (g). Within the lines, DPC 9 (534.28), JP 65 (163.96) and DPC 24 (152.55) exhibited significant positive GCA effects for seed yield whereas in testers, M3/28-3-1 (213.46) and TMV 5 (153.65) showed positive and significant GCA effects. The cross DPC 9 × M3/28-3-1 (1561.59) recorded the highest significant positive SCA effect for seed yield, followed by DPC 9 × TMV 5 (1192.19), DPC 9 × JM 6 (1088.27), JP 65 × 48-1 (706.64), YRCP 2 × JM 6 (595.06) and JP 65 ×

M3/28-3-1 (508.11). For earliness traits, the cross DPC 21 × SKI 215 (-11.23) showed the highest negative and significant SCA effect for days to 50 per cent flowering and days to maturity of the primary spike, which can be exploited for development of early maturing hybrids in castor.

Sharma *et al*. (2024) investigated the combining ability of thirteen castor genotypes over three different environments. The analysis of variance revealed that the magnitude of σ^2GCA exceeded σ^2SCA for effective length of the primary raceme and 100-seed weight (g) over environments, suggesting that these traits are mainly controlled by additive gene effects. In contrast, non-additive gene effects played a greater role in determining the number of effective branches per plant, number of capsules on the primary raceme and seed yield per plant. Among the parents, pistillate line MCP 1-1 (26.67) and testers MP 12-17 (24.26) and MP 27-17 (20.99) were found to be good general combiners for seed yield. For oil content (%), testers MP 36-17 (1.13) and MP 32-17 (0.92) showed high GCA effects. Hybrids with good SCA effect for seed yield per plant were SKP 84 × MP 36-17 (54.22), MCP 1-1 × MP 12-17 (50.23) and DPC 15 × MP 34-17 (39.82).

Kumari *et al.* (2025) evaluated four lines, ten testers and their forty hybrids produced using line × tester mating design including the standard check GCH-9 in RBD with three replications. The analysis of variance revealed that both GCA and SCA effects were significant for all traits, suggesting that the traits are influenced by both additive as well as non-additive gene actions. GCA/SCA variance ratio indicated that non-additive gene action predominated for most traits (ratio < 1), whereas additive gene action played a major role in the length of primary raceme, plant height up to primary raceme and effective length of primary raceme (ratio > 1). Parents IPC 30, JI 518, JI 531 and JI 532 were found to be good general combiners for seed yield per plant. Crosses IPC 30 × JI 533, IPC 31 × JI 532 and SKP 126 × JI 532 showed maximum significant positive SCA effects for seed yield per plant.

Pandor *et al*. (2025b) investigated combining ability for seed yield and associated characters in castor using 3 lines × 10 testers experimental design. The results revealed that GCA variance were significantly higher than SCA variance for traits such as plant height up to the primary raceme, effective number of spikes per plant, seed yield per plant, 100-seed weight (g) and oil content (%), indicating that additive gene action predominates for these traits. In contrast, In contrast, non-additive

gene action played a greater role in determining days to flowering, nodes up to the primary raceme and total length of the primary raceme. Within the parents, female lines SKP 84 and Geeta and male lines ANDCI 14, ANDCI 8, ANDCI 12-2, SKI 343 and DCS 109 showed high GCA effects for seed yield and two to three other important yield-contributing traits. Eleven hybrids exhibited positive and significant SCA effects for seed yield, with the top-performing hybrids being SKP 84 × ANDCI 14 (79.86), SKP 84 × ANDCI 10-3 (76.94), Geeta × SKI 315 (75.85), Geeta × SKI 343 (59.52) and VP 1 × DCS 97 (49.64).

12.3. Stability Analysis

Stability analysis examines how genotypes perform across different environments. Since phenotypic expression results from genotype-environment interaction, a genotype may show variable performance under changing conditions, indicating genotype × environment interaction. To explain this variation, Eberhart and Russell (1966) proposed a stability model using specific stability parameters to assess genotypic performance across environments.

Patel *et al*. (2011) studied stability parameters for eleven characters using ten inbred lines and their 45 hybrids developed through a diallel mating design across four artificially created environments. Genotype × environment interaction was significant for all traits, except the number of branches per plant. The linear component was significant for days to 50 per cent flowering, days to 50 per cent maturity, number of nodes on the main stem, stem length, effective raceme length, number of capsules on the primary raceme and seed yield per plant. Among parents, 48-1 and SKI-291 was found stable for seed yield per plant. Hybrids DCS 89 × PCS-124, 48-1 × SKI 281 and SKI 291 × SKI 215 were recorded as a stable for seed yield. On other hand SKI 291 × SKI 281, PCS 124 × SKI 291 and SKI 281 × SKI 215 were found stable in favourable environments.

Lopes *et al*. (2014) assessed the performance of 12 castor genotypes under contrasting seasonal environments (summer and winter) at low-altitude locations. Genotypes such as BRS-149 Nordestina, G1, BRS-188, Paraguacu and IAC-2226 exhibited broad adaptability and stable seed yield across the two growing seasons. Conversely, the Savannah and Lyra genotypes showed low yield and poor stability across both environments, suggesting that their productivity is highly affected by environmental factors.

Patel and Patel (2015) assessed genotype × environment interaction and stability using 16 castor genotypes across three artificially created environments for seed yield. The mean squares for both the environment and its linear component were highly significant for all the traits analyzed. Based on mean performance, unit regression and minimal deviation from regression, five genotypes GCH-4, GCH-6, GCH-7, Geeta and 48-1 were identified as stable for seed yield per plant.

Manilal (2016) evaluated 16 castor genotypes across three artificially created environments to study genotype × environment interactions and stability parameters. Within the female parents, VP-1, JP-65 and SKP-84 showed greater stability for the number of racemes per plant, maintaining consistent performance even under poor environmental conditions. The male parent 48-1 exhibited high stability and above-average performance for the percentage of pistillate whorls on secondary racemes when environmental conditions were favorable.

Chandra and Kenchanagoudar (2018) conducted an assessment of stability in castor genotypes and hybrids with respect to seed yield and associated traits. The analysis of variance conducted across 16 environments indicated significant variation among genotypes for all the traits studied. A significant genotype × environment interaction was observed for seed yield and primary raceme length. Among the 14 genotypes evaluated, GCH-6, PCH-111 and check GCH-4 exhibited stability for days to flower initiation, plant height and 100-seed weight (g).

Chaudhari *et al*. (2019) studied phenotypic stability and genotype × environment interaction using 26 castor genotypes across three environments. Partitioning of genotype × environment interaction ware found significant for effective branches per plant, 100-seed weight (g) and oil content (%) which indicated that different genotypes responded differently to the environmental conditions. The linear component of the G × E interaction was significantly higher than the non-linear component for the number of effective branches per plant, while the non-linear component predominated for 100-seed weight (g) and oil content (%). Nine genotypes *viz*., GCH-2, GCH-7, SHB-1005, SHP-1019, SHB-1029, GNCH-1, GEETA, 48-1 and JP-96 had below average stability as indicated responsive to favourable environment.

Aher *et al*. (2020) evaluated nine parental lines, 36 pistillate × pistillate hybrids and a standard check (GCH-7) over 3 environments for genotype × environment interaction and stability analysis in castor. Mean squares attributed to genotype,

genotype × environment interaction and the linear component of environments were found to be highly significant for all the characters studied. Based solely on the stability analysis, parent ANDCP-06-07 and hybrids ANDCP-06-07 × ACP-1-06-07, ANDCP-06-07 × DPC-9, VP-1 × DPC-9, DPC-9 × ANDCP-06-07-1 and ANDCP-08-01 × JP-65 showed average stability and broad adaptability across environments, whereas, the parental genotypes ACP-1-06-07, SKP-84, ANDCP-06-07-1 hybrid ACP-1-06-07 × JP-65 were well adapted to poor environments. Similarly, the hybrids ACP-06-07-1 × DPC-9, ANDCP-08-01 × ANDCP-06-07 and GCH-7 showed below-average stability but performed well under favorable environments for seed yield per plant.

Kajal and Chauhan *et al*. (2021) studied genotype × environment interaction and stability in castor for seed yield and associated traits using nine parental lines, their twenty hybrids produced using line × tester mating design and two standard checks. The mean square due to G × E interactions were significant for all traits except the number of effective branches per plant, suggesting that environmental factors had a major impact on the performance of the various genotypes. Top four hybrids *viz*., Geeta × NAUCI-8, Geeta × NAUCI-9, NAUCP-1 × NAUCI-9 and SKP-72 × NAUCI-9 were identified as a most promising and stable across environments for seed yield per plant.

The sixty-one castor genotypes including 42 hybrids, 17 parents and two checks GCH 5 and GCH-7 were evaluated by Dapke *et al.* (2023) for stability in three environments. Mean square due to both linear and non-linear components of the G x E interaction were significant for number of capsules on primary spike, seed yield per plant and 100-seed weight (g). The high magnitude of linear environmental mean squares suggests that the traits were substantially affected by the environment. Among all the parents, top five parents *viz.,* SKP-84, SKI-270, DCS-84, 48-1 and TMV-6 were average responsive (bi ≈ 1) to all the environmental conditions with higher seed yield per plant. Fourteen hybrids and checks revealed average stable response. Among them top hybrids were SKP-84 × 270, SKP-84 × TMV-6, VP-1 × SKI-270, SKP-84 × 48-1 and SKP-84 × DCS 84. Neither the parents nor the hybrids showed consistent stability for all traits across the tested environments.

Sharma *et al*. (2023) evaluated three lines, ten testers and their 30 hybrids among with one check GCH-8 over three environments in Rajasthan. Analysis of variance showed that G × E interaction was found to be significant for all the traits except 100-seed weight (g) which represented that genotypes responded differently

under different environment. Stability analysis revealed that only one parental line MP-34-17 possessed average stability for seed yield and oil content (%). Among 30 hybrids MCP-1-1 × MP-35-17 and MCP-1-1 × MP-27-17 were found suitable for seed yield per plant while, MCP-1-1 × MP-27-17 was found suitable for both seed yield and oil content (%).

12.4. Inheritance pattern of Fusarium wilt resistance

Identifying resistance sources and understanding their inheritance are key steps in breeding to develop disease-resistant crops. Fusarium wilt, resulting from *Fusarium oxysporum* f. sp. *ricini*, represents a serious soil-borne disease of castor that leads to major yield losses and is difficult to control chemically. Therefore, developing resistant varieties through breeding remains the most efficient and eco-friendly approach. Understanding the inheritance pattern of Fusarium wilt resistance helps in developing resistant lines, reducing yield losses, and ensuring sustainable disease management.

Pathak (2003) reported that studies on the genetics of wilt resistance using generation mean analysis indicated that resistance is likely governed by multiple genes (polygenes) exhibiting dominance. Both additive and non-additive genetic effects were observed to play a role in determining wilt resistance in various castor crosses.

Hanumantharao *et al*. (2005) studied the genetic control of wilt resistance in castor using F_2 segregating populations derived from two resistant sources Baker and 48-1 and two susceptible lines VI-9 and VP-1. They found that *Fusarium oxysporum* f. sp. *ricini* resistance was controlled by a single dominant gene in Baker, while in 48-1, it was regulated by two complementary genes.

Shankar *et al*. (2010) conducted inheritance studies in castor to understand the genetic control of wilt resistance using two F_2 populations of crosses *viz*., VP-1 × PCS-142 (Susceptible × Resistant) and M-574 × PCS-154 (Resistant × Susceptible). The segregation ratio (9 resistant : 7 susceptible) both F_2 populations suggested that inheritance of the resistance to wilt is controlled by two complementary genes.

Lavanya *et al*. (2011) investigated inheritance pattern of Fusarium wilt resistance using three castor crosses in wilt sick plot. The results indicated that in the cross VP-1 × 48-1, resistance to Fusarium wilt was controlled by a recessive gene, whereas in the other two crosses, DCP 13 × RG 297 and DCP 9 × RG 297, resistance exhibited incomplete dominance. The cross DPC 9 × RG 297, which involved two

resistant parents, showed a higher level of resistance compared to crosses with only one resistant parent. Wilt resistance was governed by oligogenic inheritance with epistatic interactions.

Kammili and Raoof (2014) investigated the inheritance pattern of Fusarium wilt resistance in F_2 populations derived from four crosses between resistant and susceptible parents. Their findings confirmed resistance to Fusarium wilt is controlled by digenic epistatic interactions with segregation ratios of 15:1, 9:7 and 13:3 corresponding to duplicate dominant, duplicate recessive and dominant-recessive epistasis. The mode of inheritance varied with the genetic background of the parents, emphasizing the importance of parental selection in resistance and hybrid breeding programs.

Shaw *et al.* (2018) evaluated eight F_2 populations derived from crossing between four resistant (48-1, CI-1, AP42 and AP48) and eight susceptible inbred lines for wilt resistance. Artificial screening was conducted using the sick plot method, employing a new scoring system based on days to wilt to assess the progenies' response to pathogen infection. The segregation pattern of wilt resistance in the F_2 populations varied depending on the cross. The segregation ratio in F_2 plants of the cross JI35 × 48-1 was 3 susceptible : 1 resistant, indicating that a single recessive gene governs resistance. In the F_2 populations of the crosses JC12 × 48-1, AP52 × AP48, AP72 × CI 1, AP3 × CI-1, AP130 × CI-1, and AP306 × CI-1, segregation followed a 9 susceptible : 7 resistant ratio, indicating recessive complementary gene interaction. In contrast, the cross AP134 × AP42 exhibited a 9 resistant : 7 susceptible ratio, reflecting dominant complementary gene interaction. Overall, the inheritance patterns indicate that wilt resistance is controlled either by a single gene or, in most cases, by two genes interacting complementarily.

Mohanrao *et al*. (2021) stidied the inheritance pattern of Fusarium wilt resistance using 3 F_2 populations, developed through crossing three resistant germplasm lines (AP-70, AP-127, and AP-163) with the susceptible line JI-35 in castor. They screened F_2 population in wilt sick plot. The F_2 individuals of the crosses AP-70 × JI-35 and AP-163 × JI-35 exhibited a 7 resistant : 9 susceptible segregation ratio, suggesting that two recessive genes interact complementarily to confer resistance in AP-70 and AP-163. Segregation ratio in F_2 population of cross AP-127 × JI-35 was 9

(Resistant): 7 (susceptible) indicated that two dominant genes with complementary interaction and conferring resistance of AP-127.

Deepika *et al*. (2024) studied eight F_2 populations in a sick plot to examine how Fusarium wilt resistance is inherited in castor. The genetic analysis of wilt resistance showed that YTP 1 × TMV 5 follows duplicate dominant epistasis (15 susceptible : 1 resistant), while DPC 9 × JP 65, JP 65 × SKI 215, and YRCP 1 × DPC 9 exhibit complementary epistasis (9 susceptible : 7 resistant). Monogenic recessive nature (3 Susceptible: 1 Resistant) of wilt resistance was reported in other four cross combinations *viz.,* YRCP 2 × JP 65, SKP 84 × JP 65, YRCP 2 × DPC 9 and YRCP 2 × SKP 84.

13. Materials and Methods

The current study entitled *"*Genetic architecture of seed yield, its components and Fusarium wilt resistance in castor (*Ricinus communis* L.)*"* will be conducted at the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh located in the South Saurashtra Agro-Climatic Zone-III of Gujarat. The experimental site is situated at 21.5° N latitude, 70.5° E longitude and 82.92 m above mean sea level.

The experimental material will be generation by using of six pistillate lines as a testers (female) and eight inbreds (male) as a lines. These lines and testers will be crossed in a line × tester mating design during first year (*Kharif* 2025-26) to produce F_1 hybrids. During next year (*Kharif* 2026-27), experimental materials composing 63 entries including 48 crosses, 8 parental lines, 6 testers and one standard check GCH-9 will be evaluated under three different environmental conditions created by different sowing dates as well as in sick plot condition. Simultaneously, F_2 populations will be generated for selected crosses with parental lines like resistant × resistant, resistant × susceptible, susceptible × resistant and susceptible × susceptible. These F_2 populations of four selected crosses along with their parents will be evaluated under wilt sick plot condition during third year (*Kharif* 2027-28) to investigate the inheritance of wilt resistance.

Experimental details

13.1	**Location**	**:**	Main Oilseeds Research Station, J.A.U., Junagadh
13.2	**Year and season of experiment**	**:**	• Development of crosses: *Kharif* -2025-26

			• Evaluation of experimental materials: *Kharif* -2026-27 • Study the inheritance pattern of Fusarium wilt resistance: *Kharif* -2027-28
13.3	**Number of environments**	**:**	03 E_1: 2nd fortnight of July, *Kharif* -2025-26 E_2= 2nd fortnight of August, *Kharif* -2026-27 E_3= 2nd fortnight of Sept., *Kharif* -2027-28
13.4	**Treatment details**	**:**	Total 63 entries including 8 lines + 6 testers + 48 hybrids + 1 standard check (GCH-9)
13.5	**Experimental design**	**:**	Randomized Block Design (RBD)
13.6	**Number of replications**	**:**	3

Details of Genotypes

The genotypes received from Main Oilseeds Research Station, J.A.U., Junagadh will be used in present investigation as listed below along with their pedigree and important character details.

Table 1. Genotypes used for crossing programme

Sr. No.	Name of genotypes	Pedigree	Morphological Character
Lines (Male)			
1.	JI-449	(JP-91 × PCS-124) x JI-258	G2SP-18
2.	JI-454	JP-96 × JI-376	G3SP-14
3.	JI-456	(JP-100 × JI-363) × PCS-124	G3SP-15
4.	JI-491	(JP-100 × JI-363) × PCS-124	G3SP-14
5.	JI-500	(SKP-106 × JP-105) × (JP-105 × PPL-227)	G2SP-18
6.	JI-503	(SKP-84 × JI-220) × (JP-105 × JI-291)	M2SP-14
7.	JI-553	JI-423 × RG-43	M2SP-14
8.	JI-562	Population improvement	G3SP-14
Testers (Female)			
1.	JP-96	JP-66 × 454	G3SP-17
2.	VP-1	-	G3SP-16
3.	SKP-84	SKI-1 × VP-1	M3SP-22
4.	JP-111	(SKP-106 × JP-105) × (JP-105 × PPL-277)	G2SP-16
5.	JP-115	ANDCP-08-01 × SKP-84	G3SP-18
6.	JP-116	(JP-96 × SKI-343) × (SKP-84 × SKI-352)	G3SP-15

Stem color	**:**	G	=	Green	M	=	Mohogany
Bloom	**:**	3	=	Triple	2	=	Double
Capsule	**:**	SP	=	Spiny	NSP	=	Non-spiny

13.7. Observations to be recorded

For each replication, observations will be recorded on five randomly selected competitive plants of each genotype for various characters as described below. The phenological characters namely, days to 50 per cent flowering of primary raceme, days to maturity of primary raceme, shelling out turn (%) and 100-seed weight (g) will be recorded on a plot basis. The replication wise mean values will be used for statistical analysis.

13.7.1 Days to 50 per cent flowering of primary raceme

The number of days from sowing to the appearance of 50 per cent flowering on the primary raceme in 50 per cent of the plants will be recorded.

13.7.2 Days to maturity of primary raceme

The number of days from the date of sowing to the date of physiological maturity of the primary raceme will be recorded.

13.7.3 Number of nodes up to primary raceme

At maturity, the total number of nodes from the cotyledonary node to the base of the primary spike will be recorded.

13.7.4 Plant height up to primary raceme (cm)

The plant height will be measured in centimeters from ground level to the base of the primary raceme at the time of maturity.

13.7.5 Effective length of primary raceme (cm)

Length of primary raceme covered with capsules will be measured in centimeters at the time at harvest.

13.7.6 Number of capsules on primary raceme

The total number of capsules on primary raceme will be counted at the time at harvest.

13.7.7 Number of effective branches per plant

The number of racemes bearing branches will be considered as effective branches and it will be counted at the time at harvesting.

13.7.8 Shelling out turn (%)

Well mixed 100 g capsules from bulk of five plants will be manually threshed and shelling out turn will be calculated as per following formula.

$$\text{Shelling out turn (\%)} = \frac{\text{Seed weight (g)}}{\text{Capsule weight (g)}} \times 100$$

13.7.9 100-seed weight (g)

In each replication, 100 well-filled, dried seeds will be randomly drown from the bulk produce of five selected plants of each genotype and their weight will be recorded in grams.

13.7.10 Seed yield per plant (g)

The entire effective racemes per plant will be threshed together and cleaned-dried seed will be weighed in grams.

13.7.11 Oil content (%)

A random sample of oven-dried seeds drown from the bulk produce of five selected plants of each genotype will be used to determine oil content (%) by the Nuclear Magnetic Resonance (N.M.R.) technique at the Main Oilseeds Research Station, J.A.U., Junagadh, as suggested by Tiwari et al. (1974).

13.7.12 Per cent disease incidence (%)

The reaction to wilt resistance of the entries in the field conditions (wilt sick plot) will be assessed by recording the total number of wilt infected plants at 90, 120 and 150 days after sowing. Per cent disease incidence (PDI) will be calculated using the formula suggested by McKinney, 1923.

$$\text{PDI (\%)} = \frac{\text{Number of wilt infected plants}}{\text{Total number of plants observed}} \times 100$$

14. Statistical Analysis

The data to be recorded for different characters will be subjected to the following statistical analyses:

14.1 Analysis of variance (ANOVA) for experimental design

Analysis of variance (ANOVA) for randomized block design (RBD) for each environment separately will be carried out as per Panse and Sukhatme (1985).

14.2 Line × Tester Analysis

Line × tester analysis will be carried out as per Kempthorne (1957) and Singh and Chaudhary (1985).

14.3 Estimation of heterosis

14.3.1 Heterobeltiosis (HB): The deviation of F_1 over the better parent is expressed as a percentage and will be calculated as per Fonseca and Patterson (1968).

$$\text{Heterobeltiosis (\%)} = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$\bar{F}_1$ = Mean performance of F_1 hybrid

$\overline{BP}$ = Mean performance of better parent in desired direction

14.3.2 Standard Heterosis (SH): The deviation of the F_1 hybrid over the standard check (GCH-9) is expressed as a percentage and will be worked out as per Meredith and Bridge (1972).

$$Standard\ Heterosis\ (\%) = \frac{\bar{F}_1 - \overline{SC}}{\overline{SC}} \times 100$$

Where,

$\bar{F}_1$ = Mean performance of F_1 hybrid

$\overline{SC}$ = Mean performance of the standard check GCH 9

14.4 Estimation of combining ability

Combining ability will be estimated using the method proposed by Kempthorne (1957). General combining ability (GCA) and specific combining ability (SCA) variances will be computed using covariances of half-sibs and full-sibs.

14.5 Genotype × environment interaction and stability analysis

The stability of genotypes in terms of yield and yield-related traits will be evaluated by regression analysis as described by Eberhart and Russell (1966).

14.6 Inheritance pattern of Fusarium wilt resistance in F_2 population

The Chi-square (χ^2) test developed by Karl Pearson (1900) will be used to compare observed and expected ratios to determine the type of inheritance.

The general formula of χ^2 test is as follows:

$$\chi^2 = \frac{\sum(\mathrm{O} - \mathrm{E})^2}{\mathrm{E}}$$

Where,

Σ = Summation,

O = Observed frequencies and

E = Expected frequencies

Significant χ^2 indicates a deviation from expected ratios helping identify dominant, recessive or epistatic gene action.

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